


SEQUENCE LISTING



<110> DECKERS, HARM M.
VAN ROOIJEN, GIJS
BOOTHE, JOSEPH
GOLL, JANIS
MOLONEY, MAURICE M.
DALMIA, BIPIN K.

<120> THIOREDOXIN AND THIOREDOXIN REDUCTASE CONTAINING OIL
BODY BASED PRODUCTS

<130> 034547/0104

<140> 09/897,898

<141> 2001-07-05

<150> 09/577,147

<151> 2000-05-24

<150> 09/448,600

<151> 1999-11-24

<150> 09/084,777

<151> 1998-05-27

<150> 60/047,753

<151> 1997-05-27

<150> 60/047,779

<151> 1997-05-28

<150> 60/075,863

<151> 1998-02-25

<150> 60/075,864

<151> 1998-02-25

<160> 24

<170> PatentIn Ver. 2.1

<210> 1

<211> 1002

<212> DNA

<213> Unknown Organism

<220>

<221> CDS

<222> (1)..(999)

<220>

<223> Description of Unknown Organism: Published NADPH
thioredoxin reductase

<400> 1
 atg aat ggt ctc gaa act cac aac aca agg ctc tgt atc gta gga agt 48
 Met Asn Gly Leu Glu Thr His Asn Thr Arg Leu Cys Ile Val Gly Ser
 1 5 10 15

ggc cca gcg gca cac acg gcg gcg att tac gca gct agg gct gaa ctt 96
 Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu
 20 25 30

aaa cct ctt ctc ttc gaa gga tgg atg gct aac gac atc gct ccc ggt 144
 Lys Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly
 35 40 45

ggc caa cta aca acc acc acc gac gtc gag aat ttc ccc gga ttt cca 192
 Gly Gln Leu Thr Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro
 50 55 60

gaa ggt att ctc gga gta gag ctc act gac aaa ttc cgt aaa caa tcg 240
 Glu Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser
 65 70 75 80

gag cga ttc ggt act acg ata ttt aca gag acg gtg acg aaa gtc gat 288
 Glu Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp
 85 90 95

ttc tct tcg aaa ccg ttt aag cta ttc aca gat tca aaa gcc att ctc 336
 Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu
 100 105 110

gct gac gct gtg att ctc gct act gga gct gtg gct aag cgg ctt agc 384
 Ala Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser
 115 120 125

ttc gtt gga tct ggt gaa ggt tct gga ggt ttc tgg aac cgt gga atc 432
 Phe Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile
 130 135 140

tcc gct tgt gct gtt tgc gac gga gct gct ccg ata ttc cgt aac aaa 480
 Ser Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys
 145 150 155 160

cct ctt gcg gtg atc ggt gga ggc gat tca gca atg gaa gaa gca aac 528
 Pro Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn
 165 170 175

ttt ctt aca aaa tat gga tct aaa gtg tat ata atc cat agg aga gat 576
 Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp
 180 185 190

gct ttt aga gcg tct aag att atg cag cag cga gct ttg tct aat cct 624
 Ala Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro
 195 200 205

aag att gat gtg att tgg aac tcg tct gtt gtg gaa gct tat gga gat 672
 Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp
 210 215 220

gga gaa aga gat gtg ctt gga gga ttg aaa gtg aag aat gtg gtt acc	720
Gly Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr	
225 230 235 240	
gga gat gtt tct gat tta aaa gtt tct gga ttg ttc ttt gct att ggt	768
Gly Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly	
245 250 255	
cat gag cca gct acc aag ttt ttg gat ggt ggt gtt gag tta gat tcg	816
His Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser	
260 265 270	
gat ggt tat gtt gtc acg aag cct ggt act aca cag act agc gtt ccc	864
Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro	
275 280 285	
gga gtt ttc gct gcg ggt gat gtt cag gat aag aag tat agg caa gcc	912
Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala	
290 295 300	
atc act gct gca gga act ggg tgc atg gca gct ttg gat gca gag cat	960
Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His	
305 310 315 320	
tac tta caa gag att gga tct cag caa ggt aag agt gat tga	1002
Tyr Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp	
325 330	
<210> 2	
<211> 1002	
<212> DNA	
<213> Arabidopsis sp.	
<220>	
<221> CDS	
<222> (1)..(999)	
<400> 2	
atg aat ggt ctc gaa act cac aac aca agg ctc tgt atc gta gga agt	48
Met Asn Gly Leu Glu Thr His Asn Thr Arg Leu Cys Ile Val Gly Ser	
1 5 10 15	
ggc cca gcg gca cac acg gcg gcg att tac gca gct agg gct gaa ctt	96
Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu	
20 25 30	
aaa cct ctt ctc ttc gaa gga tgg atg gct aac gac atc gct ccc ggt	144
Lys Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly	
35 40 45	
ggt caa cta aca acc acc acc gac gtc gag aat ttc ccc gga ttt cca	192
Gly Gln Leu Thr Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro	
50 55 60	
gaa ggt att ctc gga gta gag ctc act gac aaa ttc cgt aaa caa tcg	240
Glu Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser	
65 70 75 80	

gag	cga	ttc	ggt	act	acg	ata	ttt	aca	gag	acg	gtg	acg	aaa	gtc	gat	288
Glu	Arg	Phe	Gly	Thr	Thr	Ile	Phe	Thr	Glu	Thr	Val	Thr	Lys	Val	Asp	
			85						90					95		
ttc	tct	tcg	aaa	ccg	ttt	aag	cta	ttc	aca	gat	tca	aaa	gcc	att	ctc	336
Phe	Ser	Ser	Lys	Pro	Phe	Lys	Leu	Phe	Thr	Asp	Ser	Lys	Ala	Ile	Leu	
			100					105					110			
gct	gac	gct	gtg	att	ctc	gct	act	gga	gct	gtg	gct	aag	cgg	ctt	agc	384
Ala	Asp	Ala	Val	Ile	Leu	Ala	Thr	Gly	Ala	Val	Ala	Lys	Arg	Leu	Ser	
		115					120					125				
ttc	ggt	gga	tct	ggt	gaa	ggt	tct	gga	ggt	ttc	tgg	aac	cgt	gga	atc	432
Phe	Val	Gly	Ser	Gly	Glu	Gly	Ser	Gly	Gly	Phe	Trp	Asn	Arg	Gly	Ile	
	130					135					140					
tcc	gct	tgt	gct	ggt	tgc	gac	gga	gct	gct	ccg	ata	ttc	cgt	aac	aaa	480
Ser	Ala	Cys	Ala	Val	Cys	Asp	Gly	Ala	Ala	Pro	Ile	Phe	Arg	Asn	Lys	
145					150					155					160	
cct	ctt	gcg	gtg	atc	ggt	gga	ggc	gat	tca	gca	atg	gaa	gaa	gca	aac	528
Pro	Leu	Ala	Val	Ile	Gly	Gly	Gly	Asp	Ser	Ala	Met	Glu	Glu	Ala	Asn	
			165					170						175		
ttt	ctt	aca	aaa	tat	gga	tct	aaa	gtg	tat	ata	atc	cat	agg	aga	gat	576
Phe	Leu	Thr	Lys	Tyr	Gly	Ser	Lys	Val	Tyr	Ile	Ile	His	Arg	Arg	Asp	
			180					185					190			
gct	ttt	aga	gcg	tct	aag	att	atg	cag	cag	cga	gct	ttg	tct	aat	cct	624
Ala	Phe	Arg	Ala	Ser	Lys	Ile	Met	Gln	Gln	Arg	Ala	Leu	Ser	Asn	Pro	
		195					200					205				
aag	att	gat	gtg	att	tgg	aac	tcg	tct	ggt	gtg	gaa	gct	tat	gga	gat	672
Lys	Ile	Asp	Val	Ile	Trp	Asn	Ser	Ser	Val	Val	Glu	Ala	Tyr	Gly	Asp	
	210					215					220					
gga	gaa	aga	gat	gtg	ctt	gga	gga	ttg	aaa	gtg	aag	aat	gtg	ggt	acc	720
Gly	Glu	Arg	Asp	Val	Leu	Gly	Gly	Leu	Lys	Val	Lys	Asn	Val	Val	Thr	
225				230						235					240	
gga	gat	ggt	tct	gat	tta	aaa	ggt	tct	gga	ttg	ttc	ttt	gct	att	ggt	768
Gly	Asp	Val	Ser	Asp	Leu	Lys	Val	Ser	Gly	Leu	Phe	Phe	Ala	Ile	Gly	
			245					250						255		
cat	gag	cca	gct	acc	aag	ttt	ttg	gat	ggt	ggt	ggt	gag	tta	gat	tcg	816
His	Glu	Pro	Ala	Thr	Lys	Phe	Leu	Asp	Gly	Gly	Val	Glu	Leu	Asp	Ser	
		260						265					270			
gat	ggt	tat	ggt	gtc	acg	aag	cct	ggt	act	aca	cag	act	agc	ggt	ccc	864
Asp	Gly	Tyr	Val	Val	Thr	Lys	Pro	Gly	Thr	Thr	Gln	Thr	Ser	Val	Pro	
		275					280					285				
gga	ggt	ttc	gct	gcg	ggt	gat	ggt	cag	gat	aag	aag	tat	agg	caa	gcc	912
Gly	Val	Phe	Ala	Ala	Gly	Asp	Val	Gln	Asp	Lys	Lys	Tyr	Arg	Gln	Ala	
	290					295					300					

atc act gct gca gga act ggg tgc atg gca gct ttg gat gca gag cat 960
 Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His 320
 305 310 315

tac tta caa gag att gga tct cag caa ggt aag agt gat tga 1002
 Tyr Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp
 325 330

<210> 3

<211> 333

<212> PRT

<213> Arabidopsis sp.

<400> 3

Met Asn Gly Leu Glu Thr His Asn Thr Arg Leu Cys Ile Val Gly Ser
 1 5 10 15

Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu
 20 25 30

Lys Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly
 35 40 45

Gly Gln Leu Thr Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro
 50 55 60

Glu Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser
 65 70 75 80

Glu Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp
 85 90 95

Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu
 100 105 110

Ala Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser
 115 120 125

Phe Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile
 130 135 140

Ser Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys
 145 150 155 160

Pro Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn
 165 170 175

Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp
 180 185 190

Ala Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro
 195 200 205

Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp
 210 215 220

Gly Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr
 225 230 235 240
 Gly Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly
 245 250 255
 His Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser
 260 265 270
 Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro
 275 280 285
 Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala
 290 295 300
 Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His
 305 310 315 320
 Tyr Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp
 325 330

<210> 4

<211> 333

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Published NADPH
thioredoxin reductase

<400> 4

Met Asn Gly Leu Glu Thr His Asn Thr Arg Leu Cys Ile Val Gly Ser
 1 5 10 15
 Gly Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu
 20 25 30
 Lys Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly
 35 40 45
 Gly Gln Leu Thr Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro
 50 55 60
 Glu Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser
 65 70 75 80
 Glu Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp
 85 90 95
 Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu
 100 105 110
 Ala Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser
 115 120 125
 Phe Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile
 130 135 140

Ser Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys
 145 150 155 160
 Pro Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn
 165 170 175
 Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp
 180 185 190
 Ala Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro
 195 200 205
 Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp
 210 215 220
 Gly Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr
 225 230 235 240
 Gly Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly
 245 250 255
 His Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser
 260 265 270
 Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro
 275 280 285
 Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala
 290 295 300
 Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His
 305 310 315 320
 Tyr Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp
 325 330

<210> 5

<211> 3129

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (1555)..(1896)

<400> 5

ctgcaggaat tcattgtact ccagtatca ttatagtgaa agttttggct ctctcgccgg 60
 tggtttttta cctctattta aaggggtttt ccacctaaaa attctggtat cattctcact 120
 ttacttggtta ctttaatttc tcataatctt tggttgaaat tatcacgctt ccgcacacga 180
 tatccctaca aatttattat ttgttaaaca ttttcaaacc gcataaaatt ttatgaagtc 240
 ccgtctatct ttaatgtagt ctaacatttt catattgaaa tatataattt acttaatttt 300

```

agcgttggtgta gaaagcataa tgattttatc ttattcttct tcatataaat gtttaatatata 360
caatataaac aaattcttta ccttaagaag gatttcccat tttatatattt aaaaatatat 420
ttatcaaata tttttcaacc acgtaaatct cataataata agttgtttca aaagtaataa 480
aatttaactc cataattttt ttattcgact gatcttaaag caacacccag tgacacaact 540
agccattttt ttctttgaat aaaaaaatcc aattatcatt gtattttttt tataacaatga 600
aaatttcacc aaacaatcat ttgtggtatt tctgaagcaa gtcattgttat gcaaaattct 660
ataattccca tttgacacta cggaagtaac tgaagatctg cttttacatg cgagacacat 720
cttctaaagt aattttaata atagttacta tattcaagat ttcatatatc aaataactcaa 780
tattacttct aaaaaattaa ttagatataa ttaaaatatt acttttttaa ttttaagttt 840
aattggtgaa tttgtgacta ttgatttatt attctactat gtttaaattg ttttatagat 900
agtttaaagt aaatataagt aatgtagtag agtgtagag tgttacccta aaccataaac 960
tataagattt atggtggact aattttcata tatttcttat tgcttttacc ttttcttggt 1020
atgtaagtcc gtaactggaa ttactgtggg ttgccatggc actctgtggt cttttggttc 1080
atgcatggat gcttgcgcaa gaaaaagaca aagaacaaag aaaaaagaca aaacagagag 1140
acaaaacgca atcacacaac caactcaaat tagtcaactgg ctgatcaaga tcgccgcgtc 1200
catgtatgtc taaatgccat gcaaagcaac acgtgcttaa catgcacttt aaatgggtca 1260
cccatctcaa ccacacaca aacacattgc ctttttcttc atcatcacca caaccacctg 1320
tatatatcca ttctcttcg ccacctcaat ttcttcactt caacacacgt caacctgcat 1380
atgcgtgtca tcccatgccc aaatctccat gcatgttcca accaccttct ctcttatata 1440
atacctataa atacctctaa tatcactcac ttctttcacc atccatccat ccagagtact 1500
actactctac tactataata cccaaccca actcatattc aatactactc tact atg 1557
                                     Met
                                     1

gct tgc gaa gaa gga caa gtg atc gcc tgc cac acc gtt gag aca tgg 1605
Ala Ser Glu Glu Gly Gln Val Ile Ala Cys His Thr Val Glu Thr Trp
          5                      10                      15

aac gag cag ctt cag aag gct aat gaa tcc aaa act ctt gtg gtg gtt 1653
Asn Glu Gln Leu Gln Lys Ala Asn Glu Ser Lys Thr Leu Val Val Val
          20                      25                      30

gat ttc acg gct tct tgg tgt gga cca tgt cgt ttc atc gct cca ttc 1701
Asp Phe Thr Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Ala Pro Phe
          35                      40                      45

```



```

ttt gct gat ttg gct aag aaa ctt cct aac gtg ctt ttc ctc aag gtt 1749
Phe Ala Asp Leu Ala Lys Lys Leu Pro Asn Val Leu Phe Leu Lys Val
50 55 60 65

gat act gat gaa ttg aag tcg gtg gca agt gat tgg gcg ata cag gcg 1797
Asp Thr Asp Glu Leu Lys Ser Val Ala Ser Asp Trp Ala Ile Gln Ala
70 75 80

atg cca acc ttc atg ttt ttg aag gaa ggg aag att ttg gac aaa gtt 1845
Met Pro Thr Phe Met Phe Leu Lys Glu Gly Lys Ile Leu Asp Lys Val
85 90 95

gtt gga gcc aag aaa gat gag ctt cag tct acc att gcc aaa cac ttg 1893
Val Gly Ala Lys Lys Asp Glu Leu Gln Ser Thr Ile Ala Lys His Leu
100 105 110

gct taagcttaat aagtatgaac taaaatgcat gtaggtgtaa gagctcatgg 1946
Ala

agagcatgga atattgtatc cgaccatgta acagtataat aactgagctc catctcactt 2006

cttctatgaa taaacaaagg atgttatgat atattaacac tctatctatg caccttattg 2066

ttctatgata aatttcctct tattattata aatcatctga atcgtgacgg cttatggaat 2126

gcttcaaata gtacaaaaac aaatgtgtac tataagactt tctaaacaat tctaacttta 2186

gcattgtgaa cgagacataa gtgttaagaa gacataacaa ttataatgga agaagtttgt 2246

ctccatttat atattatata ttaccactt atgtattata ttaggatgtt aaggagacat 2306

aacaattata aagagagaag tttgtatcca tttatatatt atatactacc catttatata 2366

ttatacttat ccacttattt aatgtcttta taaggtttga tccatgatat ttctaattat 2426

ttagttgata tgtatatgaa agggactat ttgaactctc ttactctgta taaaggttgg 2486

atcatcctta aagtgggtct atttaatttt attgcttctt acagataaaa aaaaaattat 2546

gagttgggtt gataaaatat tgaaggattt aaaataataa taaataataa ataacatata 2606

atatatgtat ataaatttat tataatataa catttatcta taaaaaagta aatattgtca 2666

taaacttata caatcgttta gccttgctgg acgactctca attatttaaa cgagagtaaa 2726

catatttgac tttttgggta tttacaaat tattatttaa cactatatga aatttttttt 2786

ttttatcggc aaggaaataa aattaaatta ggagggacaa tgggtgtgtcc caatccttat 2846

acaaccaact tccacaggaa ggtcagggtcg gggacaacaa aaaaacaggc aagggaaatt 2906

ttttaatttg ggttgtcttg tttgctgcat aatttatgca gtaaaacact acacataacc 2966

cttttagcag tagagcaatg gttgaccgtg tgcttagctt cttttatttt atttttttat 3026

cagcaaagaa taaataaaat aaaatgagac acttcaggga tgtttcaacc cttatacaaa 3086

accccaaaaa caagtttcct agcaccctac caactaaggt acc 3129

```

<210> 6
 <211> 114
 <212> PRT
 <213> Arabidopsis thaliana

<400> 6
 Met Ala Ser Glu Glu Gly Gln Val Ile Ala Cys His Thr Val Glu Thr
 1 5 10 15
 Trp Asn Glu Gln Leu Gln Lys Ala Asn Glu Ser Lys Thr Leu Val Val
 20 25 30
 Val Asp Phe Thr Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Ala Pro
 35 40 45
 Phe Phe Ala Asp Leu Ala Lys Lys Leu Pro Asn Val Leu Phe Leu Lys
 50 55 60
 Val Asp Thr Asp Glu Leu Lys Ser Val Ala Ser Asp Trp Ala Ile Gln
 65 70 75 80
 Ala Met Pro Thr Phe Met Phe Leu Lys Glu Gly Lys Ile Leu Asp Lys
 85 90 95
 Val Val Gly Ala Lys Lys Asp Glu Leu Gln Ser Thr Ile Ala Lys His
 100 105 110
 Leu Ala

<210> 7
 <211> 3888
 <212> DNA
 <213> Unknown Organism

<220>
 <221> CDS
 <222> (1555)..(1908)

<220>
 <221> CDS
 <222> (2149)..(2655)

<220>
 <223> Description of Unknown Organism: Phaseolin
 promoter-oleosin Trxh-phaseolin terminator

<400> 7
 ctgcaggaat tcattgtact cccagtatca ttatagtgaag agtttttggt ctctcgccgg 60
 tgggtttttta cctctatttta aagggggtttt ccacctaataa attctggtat cattctcact 120
 ttacttggtta ctttaatttc tcataatctt tgggtgaaat tatcacgctt ccgcacacga 180
 tatccctaca aatttattat ttgttaaaca ttttcaaacc gcataaaatt ttatgaagtc 240

ccgtctatct ttaatgtagt ctaacatttt catattgaaa tatataattt acttaatttt 300
 agcgttggta gaaagcataa tgatttatcc ttattcttct tcatataaat gtttaatata 360
 caatataaac aaattcttta ccttaagaag gatttcccat tttatatattt aaaaatatat 420
 ttatcaaata tttttcaacc acgtaaatct cataataata agttggttca aaagtaataa 480
 aatttaactc cataattttt ttattcgact gatcttaaag caacacccag tgacacaact 540
 agccattttt ttctttgaat aaaaaaatcc aattatcatt gtattttttt tatacaatga 600
 aaatttcacc aaacaatcat ttgtggtatt tctgaagcaa gtcatgttat gcaaaattct 660
 ataattccca tttgacacta cggaagtaac tgaagatctg cttttacatg cgagacacat 720
 cttctaaagt aattttaata atagttacta tattcaagat ttcatatatc aaataactcaa 780
 tattacttct aaaaaattaa ttagatataa ttaaaatatt acttttttaa ttttaagttt 840
 aattgttgaa tttgtgacta ttgatttatt attctactat gtttaaattg ttttatagat 900
 agtttaagt aaatataagt aatgtagtag agtggttagag tgttacccta aaccataaac 960
 tataagattt atggtggact aattttcata tatttcttat tgcttttacc ttttcttggg 1020
 atgtaagtcc gtaactggaa ttactgtggg ttgccatggc actctgtggg cttttggttc 1080
 atgcatggat gcttgcgcaa gaaaaagaca aagaacaaag aaaaaagaca aaacagagag 1140
 acaaaacgca atcacacaac caactcaaat tagtcaactg ctgatcaaga tcgccgcgtc 1200
 catgtatgtc taaatgccat gcaaagcaac acgtgcttaa catgcacttt aaatgggtca 1260
 cccatctcaa cccacacaca aacacattgc ctttttcttc atcatcacca caaccacctg 1320
 tatatattca ttctcttccg ccacctcaat ttcttcactt caacacacgt caacctgcat 1380
 atgcggtgca tcccatgccc aaatctccat gcatgttcca accaccttct ctcttatata 1440
 atacctataa atacctctaa tatcactcac ttctttcatc atccatccat ccagagtact 1500
 actactctac tactataata cccaaccca actcatattc aatactactc tact atg 1557
 Met
 1
 gcg gat aca gct aga gga acc cat cac gat atc atc ggc aga gac cag 1605
 Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly Arg Asp Gln
 5 10 15
 tac ccg atg atg ggc cga gac cga gac cag tac cag atg tcc gga cga 1653
 Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly Arg
 20 25 30
 gga tct gac tac tcc aag tct agg cag att gct aaa gct gca act gct 1701
 Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr Ala
 35 40 45

gtc aca gct ggt ggt tcc ctc ctt gtt ctc tcc agc ctt acc ctt gtt	1749
Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu Val	
50 55 60 65	
gga act gtc ata gct ttg act gtt gca aca cct ctg ctc gtt atc ttc	1797
Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile Phe	
70 75 80	
agc cca atc ctt gtc ccg gct ctc atc aca gtt gca ctc ctc atc acc	1845
Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile Thr	
85 90 95	
ggt ttt ctt tcc tct gga ggg ttt ggc att gcc gct ata acc gtt ttc	1893
Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val Phe	
100 105 110	
tct tgg att tac aag taagcacaca tttatcatct tacttcataa ttttgtgcaa	1948
Ser Trp Ile Tyr Lys	
115	
tatgtgcatg catgtgttga gccagtagct ttggatcaat ttttttggtc gaataacaaa	2008
tgtacaata agaaattgca aattctaggg aacatttggt taactaaata cgaaatttga	2068
cctagctagc ttgaatgtgt ctgtgtatat catctatata ggtaaaatgc ttggtatgat	2128
acctattgat tgtgaatagg tac gca acg gga gag cac cca cag gga tca gac	2181
Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp	
120 125	
aag ttg gac agt gca agg atg aag ttg gga agc aaa gct cag gat ctg	2229
Lys Leu Asp Ser Ala Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu	
130 135 140 145	
aaa gac aga gct cag tac tac gga cag caa cat act ggt ggg gaa cat	2277
Lys Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His	
150 155 160	
gac cgt gac cgt act cgt ggt ggc cag cac act acc atg gct tcg gaa	2325
Asp Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr Met Ala Ser Glu	
165 170 175	
gaa gga caa gtg atc gcc tgc cac acc gtt gag aca tgg aac gag cag	2373
Glu Gly Gln Val Ile Ala Cys His Thr Val Glu Thr Trp Asn Glu Gln	
180 185 190	
ctt cag aag gct aat gaa tcc aaa act ctt gtg gtg gtt gat ttc acg	2421
Leu Gln Lys Ala Asn Glu Ser Lys Thr Leu Val Val Val Asp Phe Thr	
195 200 205	
gct tct tgg tgt gga cca tgt cgt ttc atc gct cca ttc ttt gct gat	2469
Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Ala Pro Phe Phe Ala Asp	
210 215 220 225	
ttg gct aag aaa ctt cct aac gtg ctt ttc ctc aag gtt gat act gat	2517
Leu Ala Lys Lys Leu Pro Asn Val Leu Phe Leu Lys Val Asp Thr Asp	
230 235 240	

```

gaa ttg aag tcg gtg gca agt gat tgg gcg ata cag gcg atg cca acc 2565
Glu Leu Lys Ser Val Ala Ser Asp Trp Ala Ile Gln Ala Met Pro Thr
      245                      250                      255

ttc atg ttt ttg aag gaa ggg aag att ttg gac aaa gtt gtt gga gcc 2613
Phe Met Phe Leu Lys Glu Gly Lys Ile Leu Asp Lys Val Val Gly Ala
      260                      265                      270

aag aaa gat gag ctt cag tct acc att gcc aaa cac ttg gct 2655
Lys Lys Asp Glu Leu Gln Ser Thr Ile Ala Lys His Leu Ala
      275                      280                      285

taagcttaat aagtatgaac taaaatgcat gtaggtgtaa gagctcatgg agagcatgga 2715
atattgtatc cgaccatgta acagtataat aactgagctc catctcactt cttctatgaa 2775
taaacaaagg atgttatgat atattaacac tctatctatg caccttattg ttctatgata 2835
aatttcctct tattattata aatcatctga atcgtgacgg cttatggaat gcttcaaata 2895
gtacaaaaac aaatgtgtac tataagactt tctaaacaat tctaacttta gcattgtgaa 2955
cgagacataa gtgttaagaa gacataacaa ttataatgga agaagtttgt ctccatttat 3015
atattatata ttaccactt atgtattata ttaggatgtt aaggagacat aacaattata 3075
aagagagaag tttgtatcca tttatatatt atatactacc catttatata ttatacttat 3135
ccacttattt aatgtcttta taaggtttga tccatgatat ttctaattatt ttagttgata 3195
tgtatatgaa aggggtactat ttgaactctc ttactctgta taaaggttgg atcatcctta 3255
aagtgggtct atttaatttt attgcttctt acagataaaa aaaaaattat gagttggttt 3315
gataaaatat tgaaggattt aaaataataa taaataataa ataacatata atatatgtat 3375
ataaatttat tataatataa catttatcta taaaaaagta aatattgtca taaatctata 3435
caatcgttta gccttgctgg acgactctca attatttaaa cgagagtaaa catatttgac 3495
tttttggtta tttaacaaat tattatttaa cactatatga aatttttttt ttttatcggc 3555
aaggaaataa aattaaatta ggagggacaa tgggtgtgtcc caatccttat acaaccaact 3615
tccacaggaa ggtcaggtcg gggacaacaa aaaaacaggc aagggaaatt ttttaatttg 3675
ggttgtcttg tttgctgcat aatttatgca gtaaaacact acacataacc ctttttagcag 3735
tagagcaatg gttgaccgtg tgcttagctt cttttatttt atttttttat cagcaaagaa 3795
taaataaaat aaaatgagac acttcaggga tgtttcaacc cttatacaaa accccaaaaa 3855
caagtttcct agcaccctac caactaaggt acc 3888

```

<210> 8

<211> 118

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Phaseolin
promoter-oleosin Trxh-phaseolin terminator

<400> 8

```

Met Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly Arg Asp
 1             5             10             15
Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly
          20             25             30
Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr
          35             40             45
Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu
          50             55             60
Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile
          65             70             75             80
Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile
          85             90             95
Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val
          100             105             110
Phe Ser Trp Ile Tyr Lys
          115

```

<210> 9

<211> 169

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Phaseolin
promoter-oleosin Trxh-phaseolin terminator

<400> 9

```

Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala
 1             5             10             15
Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln
          20             25             30
Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr
          35             40             45
Arg Gly Gly Gln His Thr Thr Met Ala Ser Glu Glu Gly Gln Val Ile
          50             55             60
Ala Cys His Thr Val Glu Thr Trp Asn Glu Gln Leu Gln Lys Ala Asn
          65             70             75             80

```

Glu Ser Lys Thr Leu Val Val Val Asp Phe Thr Ala Ser Trp Cys Gly
 85 90 95
 Pro Cys Arg Phe Ile Ala Pro Phe Phe Ala Asp Leu Ala Lys Lys Leu
 100 105 110
 Pro Asn Val Leu Phe Leu Lys Val Asp Thr Asp Glu Leu Lys Ser Val
 115 120 125
 Ala Ser Asp Trp Ala Ile Gln Ala Met Pro Thr Phe Met Phe Leu Lys
 130 135 140
 Glu Gly Lys Ile Leu Asp Lys Val Val Gly Ala Lys Lys Asp Glu Leu
 145 150 155 160
 Gln Ser Thr Ile Ala Lys His Leu Ala
 165

<210> 10
 <211> 3888
 <212> DNA
 <213> Unknown Organism

<220>
 <221> CDS
 <222> (1555)..(2250)

<220>
 <221> CDS
 <222> (2491)..(2655)

<220>
 <223> Description of Unknown Organism: Phaseolin
 promoter-Trxh oleosin-phaseolin terminator

<400> 10
 ctgcaggaat tcattgtact ccagtatca ttatagtga agttttggct ctctcgccgg 60
 tggtttttta cctctattta aaggggtttt ccacctaaaa attctgggtat cattctcact 120
 ttacttggtta ctttaatttc tcataatctt tggttgaaat tatcacgctt ccgcacacga 180
 tatccctaca aatttattat ttgttaaaca ttttcaaacc gcataaaatt ttatgaagtc 240
 ccgtctatct ttaatgtagt ctaacatttt catattgaaa tatataattt acttaatttt 300
 agcgttggta gaaagcataa tgattttatc ttattcttct tcatataaat gtttaatatata 360
 caatataaac aaattcttta ccttaagaag gatttcccat tttatatttt aaaaatatat 420
 ttatcaaata tttttcaacc acgtaaatct cataataata agttggtttca aaagtaataa 480
 aatttaactc cataattttt ttattcgact gatcttaaag caacaccag tgacacaact 540
 agccattttt ttctttgaat aaaaaaatcc aattatcatt gtattttttt tatacaatga 600

aaatttcacc	aaacaatcat	ttgtggtatt	tctgaagcaa	gtcatgttat	gcaaaaattct	660
ataattccca	tttgacacta	cggaagtaac	tgaagatctg	cttttacatg	cgagacacat	720
cttctaaagt	aattttaata	atagttacta	tattcaagat	ttcatatatc	aaataactcaa	780
tattacttct	aaaaaattaa	ttagatataa	ttaaaatatt	acttttttaa	ttttaagttt	840
aattgttgaa	tttgtgacta	ttgattttatt	attctactat	gtttaaattg	ttttatagat	900
agtttaaagt	aaatataagt	aatgtagtag	agtgttagag	tgttacccta	aaccataaac	960
tataagattt	atggtggact	aattttcata	tattttottat	tgctttttacc	ttttcttgggt	1020
atgtaagtcc	gtaactggaa	ttactgtggg	ttgccatggc	actctgtggt	cttttggttc	1080
atgcatggat	gcttgcgcaa	gaaaaagaca	aagaacaaag	aaaaaagaca	aaacagagag	1140
acaaaacgca	atcacacaac	caactcaaat	tagtcaactgg	ctgatcaaga	tcgccgcgtc	1200
catgtatgtc	taaatgccat	gcaaagcaac	acgtgcttaa	catgcacttt	aaatgggtca	1260
cccatctcaa	cccacacaca	aacacattgc	ctttttcttc	atcatcacca	caaccacctg	1320
tatatattca	ttctcttcg	ccacctcaat	ttcttcactt	caacacacgt	caacctgcat	1380
atgcgtgtca	tcccatgccc	aaatctccat	gcatgttcca	accaccttct	ctcttatata	1440
atacctataa	atacctctaa	tatcactcac	ttctttcatc	atccatccat	ccagagtact	1500
actactctac	tactataata	ccccaaccca	actcatattc	aatactactc	tact atg Met 1	1557
gct tcg gaa gaa gga caa gtg atc gcc tgc cac acc gtt gag aca tgg	Ala Ser Glu Glu Gly Gln Val Ile Ala Cys His Thr Val Glu Thr Trp	5	10	15		1605
aac gag cag ctt cag aag gct aat gaa tcc aaa act ctt gtg gtg gtt	Asn Glu Gln Leu Gln Lys Ala Asn Glu Ser Lys Thr Leu Val Val Val	20	25	30		1653
gat ttc acg gct tct tgg tgt gga cca tgt cgt ttc atc gct cca ttc	Asp Phe Thr Ala Ser Trp Cys Gly Pro Cys Arg Phe Ile Ala Pro Phe	35	40	45		1701
ttt gct gat ttg gct aag aaa ctt cct aac gtg ctt ttc ctc aag gtt	Phe Ala Asp Leu Ala Lys Lys Leu Pro Asn Val Leu Phe Leu Lys Val	50	55	60	65	1749
gat act gat gaa ttg aag tcg gtg gca agt gat tgg gcg ata cag gcg	Asp Thr Asp Glu Leu Lys Ser Val Ala Ser Asp Trp Ala Ile Gln Ala	70	75	80		1797
atg cca acc ttc atg ttt ttg aag gaa ggg aag att ttg gac aaa gtt	Met Pro Thr Phe Met Phe Leu Lys Glu Gly Lys Ile Leu Asp Lys Val	85	90	95		1845

gtt gga gcc aag aaa gat gag ctt cag tct acc att gcc aaa cac ttg 1893
 Val Gly Ala Lys Lys Asp Glu Leu Gln Ser Thr Ile Ala Lys His Leu
 100 105 110

gct atg gcg gat aca gct aga gga acc cat cac gat atc atc ggc aga 1941
 Ala Met Ala Asp Thr Ala Arg Gly Thr His His Asp Ile Ile Gly Arg
 115 120 125

gac cag tac ccg atg atg ggc cga gac cga gac cag tac cag atg tcc 1989
 Asp Gln Tyr Pro Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser
 130 135 140 145

gga cga gga tct gac tac tcc aag tct agg cag att gct aaa gct gca 2037
 Gly Arg Gly Ser Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala
 150 155 160

act gct gtc aca gct ggt ggt tcc ctc ctt gtt ctc tcc agc ctt acc 2085
 Thr Ala Val Thr Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr
 165 170 175

ctt gtt gga act gtc ata gct ttg act gtt gca aca cct ctg ctc gtt 2133
 Leu Val Gly Thr Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val
 180 185 190

atc ttc agc cca atc ctt gtc ccg gct ctc atc aca gtt gca ctc ctc 2181
 Ile Phe Ser Pro Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu
 195 200 205

atc acc ggt ttt ctt tcc tct gga ggg ttt ggc att gcc gct ata acc 2229
 Ile Thr Gly Phe Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr
 210 215 220 225

gtt ttc tct tgg att tac aag taagcacaca tttatcatct tacttcataa 2280
 Val Phe Ser Trp Ile Tyr Lys
 230

ttttgtgcaa tatgtgcatg catgtgttga gccagtagct ttggatcaat ttttttggtc 2340

gaataacaaa tgtaacaata agaaattgca aattctaggg aacatttggt taactaaata 2400

cgaaatttga cctagctagc ttgaatgtgt ctgtgtatat catctatata ggtaaaatgc 2460

ttggtatgat acctattgat tgtgaatagg tac gca acg gga gag cac cca cag 2514
 Tyr Ala Thr Gly Glu His Pro Gln
 235 240

gga tca gac aag ttg gac agt gca agg atg aag ttg gga agc aaa gct 2562
 Gly Ser Asp Lys Leu Asp Ser Ala Arg Met Lys Leu Gly Ser Lys Ala
 245 250 255

cag gat ctg aaa gac aga gct cag tac tac gga cag caa cat act ggt 2610
 Gln Asp Leu Lys Asp Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly
 260 265 270

ggg gaa cat gac cgt gac cgt act cgt ggt ggc cag cac act act 2655
 Gly Glu His Asp Arg Asp Arg Thr Arg Gly Gly Gln His Thr Thr
 275 280 285

```

taagcttaat aagtatgaac taaaatgcat gtaggtgtaa gagtcatgg agagcatgga 2715
atattgtatc cgaccatgta acagtataat aactgagctc catctcactt cttctatgaa 2775
taaacaaagg atgttatgat atattaacac tctatctatg caccttattg ttctatgata 2835
aatttcctct tattattata aatcatctga atcgtgacgg cttatggaat gcttcaaata 2895
gtacaaaaac aaatgtgtac tataagactt tctaaacaat tctaacttta gcattgtgaa 2955
cgagacataa gtgttaagaa gacataacaa ttataatgga agaagtttgt ctccatttat 3015
atattatata ttaccactt atgtattata ttaggatgtt aaggagacat aacaattata 3075
aagagagaag tttgtatcca ttatatatt atatactacc catttatata ttatacttat 3135
ccacttattt aatgtcttta taaggtttga tccatgatat ttctaataatt ttagttgata 3195
tgtatatgaa agggactat ttgaactctc ttactctgta taaaggttgg atcatcctta 3255
aagtgggtct atttaatttt attgcttctt acagataaaa aaaaaattat gagttgggtt 3315
gataaaatat tgaaggattt aaaataataa taaataataa ataacatata atatatgtat 3375
ataaatttat tataatataa catttatcta taaaaaagta aatattgtca taaatctata 3435
caatcgttta gccttgctgg acgactctca attatttaa cgagagtaaa catatttgac 3495
tttttggtta tttaacaaat tattatttaa cactatatga aaaaaaaaa ttttatcggc 3555
aaggaaataa aattaaatta ggagggacaa tgggtgtgtcc caatccttat acaaccaact 3615
tccacaggaa ggtcaggctg gggacaacaa aaaaacaggc aagggaatt ttttaatttg 3675
ggttgtcttg tttgctgcat aatttatgca gtaaaacact acacataacc ctttttagcag 3735
tagagcaatg gttgaccgtg tgcttagctt cttttatttt atttttttat cagcaaagaa 3795
taaataaaat aaaatgagac acttcaggga tgtttcaacc cttatacaaa accccaaaaa 3855
caagtttct agcaccctac caactaaggt acc 3888

```

<210> 11

<211> 232

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Phaseolin
promoter-Trxh oleosin-phaseolin terminator

<400> 11

```

Met Ala Ser Glu Glu Gly Gln Val Ile Ala Cys His Thr Val Glu Thr
  1             5             10             15

```

```

Trp Asn Glu Gln Leu Gln Lys Ala Asn Glu Ser Lys Thr Leu Val Val
      20             25             30

```

Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln
20 25 30

Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr
 35 40 45

Arg Gly Gly Gln His Thr Thr
 50 55

<210> 13

<211> 3787

<212> DNA

<213> Unknown Organism

<220>

<221> CDS

<222> (1555)..(2553)

<220>

<223> Description of Unknown Organism: Phaseolin
 promoter-thioredoxin reductase-phaseolin
 terminator

<400> 13

ctgcaggaat tcattgtact cccagtatca ttatagtga agtttttggt ctctcgccgg 60
 tgggtttttta cctctattta aaggggtttt ccacctaaaa attctggtat cattctcact 120
 ttacttggtta ctttaatttc tcataatcct tgggtgaaat tatcacgctt ccgcacacga 180
 tatccctaca aatttattat ttgttaaaca ttttcaaacc gcataaaatt ttatgaagtc 240
 ccgtctatct ttaatgtagt ctaacatttt catattgaaa tatataattt acttaatttt 300
 agcgttggtg gaaagcataa tgattttatt ttattcttct tcatataaat gtttaatat 360
 caatataaac aaattcttta ccttaagaag gatttcccat tttatatttt aaaaatatat 420
 ttatcaaata tttttcaacc acgtaaatct cataataata agttggttca aaagtaataa 480
 aatttaactc cataattttt ttattcgact gatcttaaag caacaccag tgacacaact 540
 agccattttt ttctttgaat aaaaaatcc aattatcatt gtattttttt tataaatga 600
 aaatttcacc aaacaatcat ttgtggtatt tctgaagcaa gtcattgtat gcaaaattct 660
 ataattccca tttgacacta cggaagtaac tgaagatctg cttttacatg cgagacacat 720
 cttctaaagt aattttaata atagttacta tattcaagat ttcatatatc aaataactca 780
 tattacttct aaaaaattaa ttagatataa ttaaaatatt acttttttaa ttttaagttt 840
 aattggtgaa tttgtgacta ttgatttatt attctactat gtttaaattg ttttatagat 900
 agtttaaagt aaatataagt aatgtagtag agtgtagag tgttacccta aaccataaac 960
 tataagattt atggtggact aattttcata tatttcttat tgcttttacc ttttcttggg 1020
 atgtaagtcc gtaactggaa ttactgtggg ttgccatggc actctgtggt cttttggttc 1080

atgcatggat gcttgcgcaa gaaaaagaca aagaacaaag aaaaaagaca aaacagagag																1140
acaaaacgca atcacacaac caactcaaat tagtcactgg ctgatcaaga tcgccgcgtc																1200
catgtatgtc taaatgccat gcaaagcaac acgtgcttaa catgcacttt aaatgggtca																1260
cccatctcaa cccacacaca aacacattgc cttttttcttc atcatcacca caaccacctg																1320
tatatatcca ttctcttccg ccacctcaat ttcttcaactt caacacacgt caacctgcat																1380
atgcgtgtca tcccatgccc aaatctccat gcatgttcca accaccttct ctcttatata																1440
atacctataa atacctctaa tatcactcac ttcttttcac atccatccat ccagagtact																1500
actactctac tactataata cccaaccca actcatattc aatactactc tact atg																1557
																Met
																1
aat ggt ctc gaa act cac aac aca agg ctc tgt atc gta gga agt ggc																1605
Asn Gly Leu Glu Thr His Asn Thr Arg Leu Cys Ile Val Gly Ser Gly																
																5
																10
																15
cca gcg gca cac acg gcg gcg att tac gca gct agg gct gaa ctt aaa																1653
Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu Lys																
																20
																25
																30
cct ctt ctc ttc gaa gga tgg atg gct aac gac atc gct ccc ggt ggt																1701
Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly Gly																
																35
																40
																45
caa cta aca acc acc acc gac gtc gag aat ttc ccc gga ttt cca gaa																1749
Gln Leu Thr Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro Glu																
																50
																55
																60
																65
ggt att ctc gga gta gag ctc act gac aaa ttc cgt aaa caa tcg gag																1797
Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser Glu																
																70
																75
																80
cga ttc ggt act acg ata ttt aca gag acg gtg acg aaa gtc gat ttc																1845
Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp Phe																
																85
																90
																95
tct tcg aaa ccg ttt aag cta ttc aca gat tca aaa gcc att ctc gct																1893
Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu Ala																
																100
																105
																110
gac gct gtg att ctc gct act gga gct gtg gct aag cgg ctt agc ttc																1941
Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser Phe																
																115
																120
																125
gtt gga tct ggt gaa ggt tct gga ggt ttc tgg aac cgt gga atc tcc																1989
Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile Ser																
																130
																135
																140
																145
gct tgt gct gtt tgc gac gga gct gct ccg ata ttc cgt aac aaa cct																2037
Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys Pro																
																150
																155
																160

ctt gcg gtg atc ggt gga ggc gat tca gca atg gaa gaa gca aac ttt	2085
Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn Phe	
165 170 175	
ctt aca aaa tat gga tct aaa gtg tat ata atc cat agg aga gat gct	2133
Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp Ala	
180 185 190	
ttt aga gcg tct aag att atg cag cag cga gct ttg tct aat cct aag	2181
Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro Lys	
195 200 205	
att gat gtg att tgg aac tcg tct gtt gtg gaa gct tat gga gat gga	2229
Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp Gly	
210 215 220 225	
gaa aga gat gtg ctt gga gga ttg aaa gtg aag aat gtg gtt acc gga	2277
Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr Gly	
230 235 240	
gat gtt tct gat tta aaa gtt tct gga ttg ttc ttt gct att ggt cat	2325
Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly His	
245 250 255	
gag cca gct acc aag ttt ttg gat ggt ggt gtt gag tta gat tcg gat	2373
Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser Asp	
260 265 270	
ggt tat gtt gtc acg aag cct ggt act aca cag act agc gtt ccc gga	2421
Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro Gly	
275 280 285	
ggt ttc gct gcg ggt gat gtt cag gat aag aag tat agg caa gcc atc	2469
Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala Ile	
290 295 300 305	
act gct gca gga act ggg tgc atg gca gct ttg gat gca gag cat tac	2517
Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His Tyr	
310 315 320	
tta caa gag att gga tct cag caa ggt aag agt gat tgaagcttaa	2563
Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp	
325 330	
taagtatgaa ctaaaatgca tgtaggtgta agagctcatg gagagcatgg aatattgtat	2623
ccgaccatgt aacagtataa taactgagct ccattctact tcttctatga ataaacaaag	2683
gatgttatga tatattaaca ctctatctat gcaccttatt gttctatgat aaatttcctc	2743
ttattattat aaatcatctg aatcgtgacg gcttatggaa tgcttcaaag agtacaaaaa	2803
caaatgtgta ctataagact ttctaaacaa ttctaacttt agcattgtga acgagacata	2863
agtgttaaga agacataaca attataatgg aagaagtttg tctccattta tatattatat	2923
attaccact tatgtattat attaggatgt taaggagaca taacaattat aaagagagaa	2983

gtttgtatcc atttatatat tatatactac ccatttatat attatactta tccacttatt 3043
 taatgtcttt ataagggttg atccatgata tttctaatat tttagttgat atgtatatga 3103
 aagggtacta tttgaactct cttactctgt ataaagggtg gatcatcctt aaagtgggtc 3163
 tatttaattt tattgcttct tacagataaa aaaaaaatta tgagttgggtt tgataaaata 3223
 ttgaaggatt taaaataata ataaataata aataacatat aatatatgta tataaattta 3283
 ttataatata acatttatct ataaaaaagt aaatattgtc ataaatctat acaatcggtt 3343
 agccttgctg gacgactctc aattatttaa acgagagtaa acatatttga ctttttggtt 3403
 atttaacaaa ttattattta acactatatg aaattttttt tttttatcgg caaggaaata 3463
 aaattaaatt aggagggaca atggtgtgtc ccaatcctta tacaaccaac ttccacagga 3523
 aggtcaggtc ggggacaaca aaaaaacagg caagggaat tttttaattt gggttgtctt 3583
 gtttgctgca taatttatgc agtaaaacac tacacataac ctttttagca gtagagcaat 3643
 ggttgaccgt gtgcttagct tcttttattt ttttttttta tcagcaaaga ataaataaaa 3703
 taaaatgaga cacttcaggg atgtttcaac cttatacaa aaccccaaaa acaagtttcc 3763
 tagcaccta ccaactaagg tacc 3787

<210> 14

<211> 333

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Phaseolin
 promoter-thioredoxin reductase-phaseolin
 terminator

<400> 14

Met	Asn	Gly	Leu	Glu	Thr	His	Asn	Thr	Arg	Leu	Cys	Ile	Val	Gly	Ser
1				5					10					15	
Gly	Pro	Ala	Ala	His	Thr	Ala	Ala	Ile	Tyr	Ala	Ala	Arg	Ala	Glu	Leu
			20					25					30		
Lys	Pro	Leu	Leu	Phe	Glu	Gly	Trp	Met	Ala	Asn	Asp	Ile	Ala	Pro	Gly
		35					40					45			
Gly	Gln	Leu	Thr	Thr	Thr	Thr	Asp	Val	Glu	Asn	Phe	Pro	Gly	Phe	Pro
	50					55					60				
Glu	Gly	Ile	Leu	Gly	Val	Glu	Leu	Thr	Asp	Lys	Phe	Arg	Lys	Gln	Ser
65				70						75				80	
Glu	Arg	Phe	Gly	Thr	Thr	Ile	Phe	Thr	Glu	Thr	Val	Thr	Lys	Val	Asp
				85					90					95	

Phe Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu
 100 105 110
 Ala Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser
 115 120 125
 Phe Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile
 130 135 140
 Ser Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys
 145 150 155 160
 Pro Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn
 165 170 175
 Phe Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp
 180 185 190
 Ala Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro
 195 200 205
 Lys Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp
 210 215 220
 Gly Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr
 225 230 235 240
 Gly Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly
 245 250 255
 His Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser
 260 265 270
 Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro
 275 280 285
 Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala
 290 295 300
 Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His
 305 310 315 320
 Tyr Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp
 325 330

<210> 15
 <211> 4546
 <212> DNA
 <213> Unknown Organism

<220>
 <221> CDS
 <222> (1555)..(1908)

<220>
 <221> CDS
 <222> (2149)..(3312)

<220>
 <223> Description of Unknown Organism: Phaseolin
 promoter-oleosin thioredoxin reductase-phaseolin
 terminator

<400> 15
 ctgcaggaat tcattgtact cccagtatca ttatagtga agttttggct ctctcgccgg 60
 tgggtttttta cctctattta aaggggtttt ccacctaaaa attctgggtat cattctcact 120
 ttacttggtta ctttaatttc tcataatctt tgggtgaaat tatcacgctt ccgcacacga 180
 tatccctaca aatttattat ttgttaaaca ttttcaaacc gcataaaatt ttatgaagtc 240
 ccgtctatct ttaatgtagt ctaacatttt catattgaaa tatataattt acttaatttt 300
 agcgttggtg gaaagcataa tgatttatct ttattcttct tcatataaat gtttaatatata 360
 caatataaac aaattcttta ccttaagaag gatttcccat tttatatattt aaaaatatat 420
 ttatcaaata tttttcaacc acgtaaatct cataataata agttgtttca aaagtaataa 480
 aatttaactc cataattttt ttattcgact gatcttaaag caacacccag tgacacaact 540
 agccattttt ttctttgaat aaaaaaatcc aattatcatt gtattttttt tatacaatga 600
 aaatttcacc aaacaatcat ttgtggtatt tctgaagcaa gtcattgttat gcaaaattct 660
 ataattccca ttgacacta cggaagtaac tgaagatctg cttttacatg cgagacacat 720
 cttctaaagt aattttaata atagtacta tattcaagat ttcatatatc aaataactca 780
 tattacttct aaaaaattaa ttagatataa ttaaaatatt acttttttaa ttttaagttt 840
 aattgttgaa tttgtgacta ttgatttatt attctactat gtttaaattg ttttatagat 900
 agtttaaagt aaatataagt aatgtagtag agtggttagag tgttacccta aaccataaac 960
 tataagattt atgggtggact aattttcata tatttcttat tgcttttacc ttttcttggg 1020
 atgtaagtcc gtaactggaa ttactgtggg ttgcatggc actctgtggg cttttgggtc 1080
 atgcatggat gcttgcgcaa gaaaaagaca aagaacaaag aaaaaagaca aaacagagag 1140
 acaaaacgca atcacacaac caactcaaat tagtcaactgg ctgatcaaga tcgccgcgctc 1200
 catgtatgtc taaatgccat gcaaagcaac acgtgcttaa catgcacttt aaatgggtca 1260
 cccatctcaa cccacacaca aacacattgc ctttttcttc atcatcacca caaccacctg 1320
 tatatatcca ttctcttccg ccacctcaat ttcttcactt caacacacgt caacctgcat 1380
 atgcgtgtca tcccatgcc aaatctccat gcatgttcca accaccttct ctcttatata 1440

gac	cgt	gac	cgt	act	cgt	ggt	ggc	cag	cac	act	acc	atg	aat	ggt	ctc	2325
Asp	Arg	Asp	Arg	Thr	Arg	Gly	Gly	Gln	His	Thr	Thr	Met	Asn	Gly	Leu	
			165					170					175			
gaa	act	cac	aac	aca	agg	ctc	tgt	atc	gta	gga	agt	ggc	cca	gcg	gca	2373
Glu	Thr	His	Asn	Thr	Arg	Leu	Cys	Ile	Val	Gly	Ser	Gly	Pro	Ala	Ala	
		180					185					190				
cac	acg	gcg	gcg	att	tac	gca	gct	agg	gct	gaa	ctt	aaa	cct	ctt	ctc	2421
His	Thr	Ala	Ala	Ile	Tyr	Ala	Ala	Arg	Ala	Glu	Leu	Lys	Pro	Leu	Leu	
	195					200					205					
ttc	gaa	gga	tgg	atg	gct	aac	gac	atc	gct	ccc	ggt	ggt	caa	cta	aca	2469
Phe	Glu	Gly	Trp	Met	Ala	Asn	Asp	Ile	Ala	Pro	Gly	Gly	Gln	Leu	Thr	
210					215					220					225	
acc	acc	acc	gac	gtc	gag	aat	ttc	ccc	gga	ttt	cca	gaa	ggt	att	ctc	2517
Thr	Thr	Thr	Asp	Val	Glu	Asn	Phe	Pro	Gly	Phe	Pro	Glu	Gly	Ile	Leu	
			230					235						240		
gga	gta	gag	ctc	act	gac	aaa	ttc	cgt	aaa	caa	tcg	gag	cga	ttc	ggt	2565
Gly	Val	Glu	Leu	Thr	Asp	Lys	Phe	Arg	Lys	Gln	Ser	Glu	Arg	Phe	Gly	
			245					250					255			
act	acg	ata	ttt	aca	gag	acg	gtg	acg	aaa	gtc	gat	ttc	tct	tcg	aaa	2613
Thr	Thr	Ile	Phe	Thr	Glu	Thr	Val	Thr	Lys	Val	Asp	Phe	Ser	Ser	Lys	
		260					265					270				
ccg	ttt	aag	cta	ttc	aca	gat	tca	aaa	gcc	att	ctc	gct	gac	gct	gtg	2661
Pro	Phe	Lys	Leu	Phe	Thr	Asp	Ser	Lys	Ala	Ile	Leu	Ala	Asp	Ala	Val	
	275					280					285					
att	ctc	gct	act	gga	gct	gtg	gct	aag	cgg	ctt	agc	ttc	gtt	gga	tct	2709
Ile	Leu	Ala	Thr	Gly	Ala	Val	Ala	Lys	Arg	Leu	Ser	Phe	Val	Gly	Ser	
290					295					300					305	
ggt	gaa	ggt	tct	gga	ggt	ttc	tgg	aac	cgt	gga	atc	tcc	gct	tgt	gct	2757
Gly	Glu	Gly	Ser	Gly	Gly	Phe	Trp	Asn	Arg	Gly	Ile	Ser	Ala	Cys	Ala	
			310					315						320		
gtt	tgc	gac	gga	gct	gct	ccg	ata	ttc	cgt	aac	aaa	cct	ctt	gcg	gtg	2805
Val	Cys	Asp	Gly	Ala	Ala	Pro	Ile	Phe	Arg	Asn	Lys	Pro	Leu	Ala	Val	
			325					330					335			
atc	ggt	gga	ggc	gat	tca	gca	atg	gaa	gaa	gca	aac	ttt	ctt	aca	aaa	2853
Ile	Gly	Gly	Gly	Asp	Ser	Ala	Met	Glu	Glu	Ala	Asn	Phe	Leu	Thr	Lys	
			340				345					350				
tat	gga	tct	aaa	gtg	tat	ata	atc	cat	agg	aga	gat	gct	ttt	aga	gcg	2901
Tyr	Gly	Ser	Lys	Val	Tyr	Ile	Ile	His	Arg	Arg	Asp	Ala	Phe	Arg	Ala	
	355					360					365					
tct	aag	att	atg	cag	cag	cga	gct	ttg	tct	aat	cct	aag	att	gat	gtg	2949
Ser	Lys	Ile	Met	Gln	Gln	Arg	Ala	Leu	Ser	Asn	Pro	Lys	Ile	Asp	Val	
370					375					380					385	

att tgg aac tcg tct gtt gtg gaa gct tat gga gat gga gaa aga gat 2997
 Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp Gly Glu Arg Asp
 390 395 400

gtg ctt gga gga ttg aaa gtg aag aat gtg gtt acc gga gat gtt tct 3045
 Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr Gly Asp Val Ser
 405 410 415

gat tta aaa gtt tct gga ttg ttc ttt gct att ggt cat gag cca gct 3093
 Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly His Glu Pro Ala
 420 425 430

acc aag ttt ttg gat ggt ggt gtt gag tta gat tcg gat ggt tat gtt 3141
 Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser Asp Gly Tyr Val
 435 440 445

gtc acg aag cct ggt act aca cag act agc gtt ccc gga gtt ttc gct 3189
 Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro Gly Val Phe Ala
 450 455 460 465

gcg ggt gat gtt cag gat aag aag tat agg caa gcc atc act gct gca 3237
 Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala Ile Thr Ala Ala
 470 475 480

gga act ggg tgc atg gca gct ttg gat gca gag cat tac tta caa gag 3285
 Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His Tyr Leu Gln Glu
 485 490 495

att gga tct cag caa ggt aag agt gat tgaagcttaa taagtatgaa 3332
 Ile Gly Ser Gln Gln Gly Lys Ser Asp
 500 505

ctaaaatgca tgtaggtgta agagctcatg gagagcatgg aatattgtat ccgaccatgt 3392

aacagtataa taactgagct ccatctcact tcttctatga ataaacaaag gatgttatga 3452

tatattaaca ctctatctat gcaccttatt gttctatgat aaatttcctc ttattattat 3512

aaatcatctg aatcgtgacg gcttatggaa tgcttcaa atgtacaaaaa caaatgtgta 3572

ctataagact ttctaataaa ttctaacttt agcattgtga acgagacata agtggttaaga 3632

agacataaca attataatgg aagaagtttg tctccattta tatattatat attaccact 3692

tatgtattat attaggatgt taaggagaca taacaattat aaagagagaa gtttgtatcc 3752

atttatatat tatatactac ccatttatat attatactta tccacttatt taatgtcttt 3812

ataagggttg atccatgata tttctaatat tttagttgat atgtatatga aagggtacta 3872

tttgaactct ctactctgt ataaaggttg gatcatcctt aaagtgggtc tatttaattt 3932

tattgcttct tacagataaa aaaaaaatta tgagttggtt tgataaaata ttgaaggatt 3992

taaaataata ataaataata aataacatat aatatatgta tataaattta ttataatata 4052

acatttatct ataaaaaagt aaatattgtc ataaatctat acaatcgttt agccttgctg 4112

gacgactctc aattattttaa acgagagtaa acatatttga ctttttggtt atttaacaaa 4172
 ttattatttta acactatatg aaattttttt tttttatcgg caaggaaata aaattaaatt 4232
 aggagggaca atggtgtgtc ccaatcctta tacaaccaac ttccacagga aggtcaggtc 4292
 ggggacaaca aaaaaacagg caagggaaat tttttaattt gggttgtctt gtttgctgca 4352
 taatttatgc agtaaaacac tacacataac ccttttagca gtagagcaat ggttgaccgt 4412
 gtgcttagct tcttttattt tattttttta tcagcaaaga ataaataaaa taaaatgaga 4472
 cacttcaggg atgtttcaac ccttatacaa aaccccaaaa acaagtttcc tagcacccta 4532
 ccaactaagg tacc 4546

<210> 16

<211> 118

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Phaseolin
 promoter-oleosin thioredoxin reductase-phaseolin
 terminator

<400> 16

Met	Ala	Asp	Thr	Ala	Arg	Gly	Thr	His	His	Asp	Ile	Ile	Gly	Arg	Asp
1				5				10					15		
Gln	Tyr	Pro	Met	Met	Gly	Arg	Asp	Arg	Asp	Gln	Tyr	Gln	Met	Ser	Gly
			20					25					30		
Arg	Gly	Ser	Asp	Tyr	Ser	Lys	Ser	Arg	Gln	Ile	Ala	Lys	Ala	Ala	Thr
			35					40					45		
Ala	Val	Thr	Ala	Gly	Gly	Ser	Leu	Leu	Val	Leu	Ser	Ser	Leu	Thr	Leu
			50				55					60			
Val	Gly	Thr	Val	Ile	Ala	Leu	Thr	Val	Ala	Thr	Pro	Leu	Leu	Val	Ile
			65			70				75				80	
Phe	Ser	Pro	Ile	Leu	Val	Pro	Ala	Leu	Ile	Thr	Val	Ala	Leu	Leu	Ile
				85					90					95	
Thr	Gly	Phe	Leu	Ser	Ser	Gly	Gly	Phe	Gly	Ile	Ala	Ala	Ile	Thr	Val
			100					105					110		
Phe	Ser	Trp	Ile	Tyr	Lys										
			115												

<210> 17

<211> 388

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Phaseolin
promoter-oleosin thioredoxin reductase-phaseolin
terminator

<400> 17

Tyr	Ala	Thr	Gly	Glu	His	Pro	Gln	Gly	Ser	Asp	Lys	Leu	Asp	Ser	Ala	1	5	10	15
Arg	Met	Lys	Leu	Gly	Ser	Lys	Ala	Gln	Asp	Leu	Lys	Asp	Arg	Ala	Gln	20	25	30	
Tyr	Tyr	Gly	Gln	Gln	His	Thr	Gly	Gly	Glu	His	Asp	Arg	Asp	Arg	Thr	35	40	45	
Arg	Gly	Gly	Gln	His	Thr	Thr	Met	Asn	Gly	Leu	Glu	Thr	His	Asn	Thr	50	55	60	
Arg	Leu	Cys	Ile	Val	Gly	Ser	Gly	Pro	Ala	Ala	His	Thr	Ala	Ala	Ile	65	70	75	80
Tyr	Ala	Ala	Arg	Ala	Glu	Leu	Lys	Pro	Leu	Leu	Phe	Glu	Gly	Trp	Met	85	90	95	
Ala	Asn	Asp	Ile	Ala	Pro	Gly	Gly	Gln	Leu	Thr	Thr	Thr	Thr	Asp	Val	100	105	110	
Glu	Asn	Phe	Pro	Gly	Phe	Pro	Glu	Gly	Ile	Leu	Gly	Val	Glu	Leu	Thr	115	120	125	
Asp	Lys	Phe	Arg	Lys	Gln	Ser	Glu	Arg	Phe	Gly	Thr	Thr	Ile	Phe	Thr	130	135	140	
Glu	Thr	Val	Thr	Lys	Val	Asp	Phe	Ser	Ser	Lys	Pro	Phe	Lys	Leu	Phe	145	150	155	160
Thr	Asp	Ser	Lys	Ala	Ile	Leu	Ala	Asp	Ala	Val	Ile	Leu	Ala	Thr	Gly	165	170	175	
Ala	Val	Ala	Lys	Arg	Leu	Ser	Phe	Val	Gly	Ser	Gly	Glu	Gly	Ser	Gly	180	185	190	
Gly	Phe	Trp	Asn	Arg	Gly	Ile	Ser	Ala	Cys	Ala	Val	Cys	Asp	Gly	Ala	195	200	205	
Ala	Pro	Ile	Phe	Arg	Asn	Lys	Pro	Leu	Ala	Val	Ile	Gly	Gly	Gly	Asp	210	215	220	
Ser	Ala	Met	Glu	Glu	Ala	Asn	Phe	Leu	Thr	Lys	Tyr	Gly	Ser	Lys	Val	225	230	235	240
Tyr	Ile	Ile	His	Arg	Arg	Asp	Ala	Phe	Arg	Ala	Ser	Lys	Ile	Met	Gln	245	250	255	
Gln	Arg	Ala	Leu	Ser	Asn	Pro	Lys	Ile	Asp	Val	Ile	Trp	Asn	Ser	Ser	260	265	270	

Val Val Glu Ala Tyr Gly Asp Gly Glu Arg Asp Val Leu Gly Gly Leu
 275 280 285

Lys Val Lys Asn Val Val Thr Gly Asp Val Ser Asp Leu Lys Val Ser
 290 295 300

Gly Leu Phe Phe Ala Ile Gly His Glu Pro Ala Thr Lys Phe Leu Asp
 305 310 315 320

Gly Gly Val Glu Leu Asp Ser Asp Gly Tyr Val Val Thr Lys Pro Gly
 325 330 335

Thr Thr Gln Thr Ser Val Pro Gly Val Phe Ala Ala Gly Asp Val Gln
 340 345 350

Asp Lys Lys Tyr Arg Gln Ala Ile Thr Ala Ala Gly Thr Gly Cys Met
 355 360 365

Ala Ala Leu Asp Ala Glu His Tyr Leu Gln Glu Ile Gly Ser Gln Gln
 370 375 380

Gly Lys Ser Asp
 385

<210> 18
 <211> 4545
 <212> DNA
 <213> Unknown Organism

<220>
 <221> CDS
 <222> (1555)..(2907)

<220>
 <221> CDS
 <222> (3148)..(3312)

<220>
 <223> Description of Unknown Organism: Phaseolin
 promoter-thioredoxin reductase oleosin-phaseolin
 terminator

<400> 18
 ctgcaggaat tcattgtact ccagtatca ttatagtga agttttggct ctctcgccgg 60
 tggtttttta cctctattta aaggggtttt ccacataaaa attctggtat cattctcact 120
 ttacttggtta ctttaatttc tcataatctt tggttgaaat tatcacgctt ccgcacacga 180
 tatccctaca aatttattat ttgttaaaca ttttcaaacc gcataaaatt ttatgaagtc 240
 ccgtctatct ttaatgtagt ctaacatttt catattgaaa tatataattt acttaatttt 300
 agcgttggtg gaaagcataa tgatttattc ttattcttct tcatataaat gttaaatata 360
 caatataaac aaattcttta ccttaagaag gatttcccat tttatatttt aaaaatatat 420

```

ttatcaaata tttttcaacc acgtaaatct cataataata agttgtttca aaagtaataa 480
aatttaactc cataattttt ttattcgact gatcttaaag caacacccag tgacacaact 540
agccattttt ttctttgaat aaaaaaatcc aattatcatt gtattttttt tatacaatga 600
aaatttcacc aaacaatcat ttgtggtatt tctgaagcaa gtcattgttat gcaaaattct 660
ataattccca ttgacacta cggaagtaac tgaagatctg cttttacatg cgagacacat 720
cttctaaagt aattttaata atagttacta tattcaagat ttcatatatc aaatactcaa 780
tattactttc aaaaaattaa ttagatataa ttaaaatatt acttttttaa ttttaagttt 840
aattgttgaa ttgtgacta ttgatttatt attctactat gtttaaattg ttttatagat 900
agtttaaagt aaatataagt aatgtagtag agtgtagag tgttacccta aaccataaac 960
tataagattt atggtggact aattttcata tatttcttat tgcttttacc ttttcttggg 1020
atgtaagtcc gtaactggaa ttactgtggg ttgccatggc actctgtggg cttttgggtc 1080
atgcatggat gcttgcgcaa gaaaaagaca aagaacaaag aaaaaagaca aaacagagag 1140
acaaaacgca atcacacaac caactcaaat tagtcactgg ctgatcaaga tcgccgcgtc 1200
catgtatgtc taaatgccat gcaaagcaac acgtgcttaa catgcacttt aaatgggtca 1260
cccatctcaa cccacacaca aacacattgc ctttttcttc atcatcacca caaccacctg 1320
tatatatcca ttctcttcgg ccacctcaat ttcttcactt caacacacgt caacctgcat 1380
atgcgtgtca tcccatgccc aaatctccat gcatgttcca accaccttct ctcttatata 1440
atacctataa atacctctaa tatcactcac ttctttcatc atccatccat ccagagtact 1500
actactctac tactataata cccaaccca actcatattc aatactactc tact atg 1557
                                     Met
                                     1

aat ggt ctc gaa act cac aac aca agg ctc tgt atc gta gga agt ggc 1605
Asn Gly Leu Glu Thr His Asn Thr Arg Leu Cys Ile Val Gly Ser Gly
      5                      10                      15

cca gcg gca cac acg gcg gcg att tac gca gct agg gct gaa ctt aaa 1653
Pro Ala Ala His Thr Ala Ala Ile Tyr Ala Ala Arg Ala Glu Leu Lys
      20                      25                      30

cct ctt ctc ttc gaa gga tgg atg gct aac gac atc gct ccc ggt ggt 1701
Pro Leu Leu Phe Glu Gly Trp Met Ala Asn Asp Ile Ala Pro Gly Gly
      35                      40                      45

caa cta aca acc acc acc gac gtc gag aat ttc ccc gga ttt cca gaa 1749
Gln Leu Thr Thr Thr Thr Asp Val Glu Asn Phe Pro Gly Phe Pro Glu
      50                      55                      60                      65

```


ggt att ctc gga gta gag ctc act gac aaa ttc cgt aaa caa tcg gag	1797
Gly Ile Leu Gly Val Glu Leu Thr Asp Lys Phe Arg Lys Gln Ser Glu	
70 75 80	
cga ttc ggt act acg ata ttt aca gag acg gtg acg aaa gtc gat ttc	1845
Arg Phe Gly Thr Thr Ile Phe Thr Glu Thr Val Thr Lys Val Asp Phe	
85 90 95	
tct tcg aaa ccg ttt aag cta ttc aca gat tca aaa gcc att ctc gct	1893
Ser Ser Lys Pro Phe Lys Leu Phe Thr Asp Ser Lys Ala Ile Leu Ala	
100 105 110	
gac gct gtg att ctc gct act gga gct gtg gct aag cgg ctt agc ttc	1941
Asp Ala Val Ile Leu Ala Thr Gly Ala Val Ala Lys Arg Leu Ser Phe	
115 120 125	
gtt gga tct ggt gaa ggt tct gga ggt ttc tgg aac cgt gga atc tcc	1989
Val Gly Ser Gly Glu Gly Ser Gly Gly Phe Trp Asn Arg Gly Ile Ser	
130 135 140 145	
gct tgt gct gtt tgc gac gga gct gct ccg ata ttc cgt aac aaa cct	2037
Ala Cys Ala Val Cys Asp Gly Ala Ala Pro Ile Phe Arg Asn Lys Pro	
150 155 160	
ctt gcg gtg atc ggt gga ggc gat tca gca atg gaa gaa gca aac ttt	2085
Leu Ala Val Ile Gly Gly Gly Asp Ser Ala Met Glu Glu Ala Asn Phe	
165 170 175	
ctt aca aaa tat gga tct aaa gtg tat ata atc cat agg aga gat gct	2133
Leu Thr Lys Tyr Gly Ser Lys Val Tyr Ile Ile His Arg Arg Asp Ala	
180 185 190	
ttt aga gcg tct aag att atg cag cag cga gct ttg tct aat cct aag	2181
Phe Arg Ala Ser Lys Ile Met Gln Gln Arg Ala Leu Ser Asn Pro Lys	
195 200 205	
att gat gtg att tgg aac tcg tct gtt gtg gaa gct tat gga gat gga	2229
Ile Asp Val Ile Trp Asn Ser Ser Val Val Glu Ala Tyr Gly Asp Gly	
210 215 220 225	
gaa aga gat gtg ctt gga gga ttg aaa gtg aag aat gtg gtt acc gga	2277
Glu Arg Asp Val Leu Gly Gly Leu Lys Val Lys Asn Val Val Thr Gly	
230 235 240	
gat gtt tct gat tta aaa gtt tct gga ttg ttc ttt gct att ggt cat	2325
Asp Val Ser Asp Leu Lys Val Ser Gly Leu Phe Phe Ala Ile Gly His	
245 250 255	
gag cca gct acc aag ttt ttg gat ggt ggt gtt gag tta gat tcg gat	2373
Glu Pro Ala Thr Lys Phe Leu Asp Gly Gly Val Glu Leu Asp Ser Asp	
260 265 270	
ggt tat gtt gtc acg aag cct ggt act aca cag act agc gtt ccc gga	2421
Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro Gly	
275 280 285	

ggt ttc gct gcg ggt gat gtt cag gat aag aag tat agg caa gcc atc	2469
Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala Ile	
290 295 300 305	
act gct gca gga act ggg tgc atg gca gct ttg gat gca gag cat tac	2517
Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His Tyr	
310 315 320	
tta caa gag att gga tct cag caa ggt aag agt gat atg gcg gat aca	2565
Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp Met Ala Asp Thr	
325 330 335	
gct aga gga acc cat cac gat atc atc ggc aga gac cag tac ccg atg	2613
Ala Arg Gly Thr His His Asp Ile Ile Gly Arg Asp Gln Tyr Pro Met	
340 345 350	
atg ggc cga gac cga gac cag tac cag atg tcc gga cga gga tct gac	2661
Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly Arg Gly Ser Asp	
355 360 365	
tac tcc aag tct agg cag att gct aaa gct gca act gct gtc aca gct	2709
Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr Ala Val Thr Ala	
370 375 380 385	
ggt ggt tcc ctc ctt gtt ctc tcc agc ctt acc ctt gtt gga act gtc	2757
Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu Val Gly Thr Val	
390 395 400	
ata gct ttg act gtt gca aca cct ctg ctc gtt atc ttc agc cca atc	2805
Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile Phe Ser Pro Ile	
405 410 415	
ctt gtc ccg gct ctc atc aca gtt gca ctc ctc atc acc ggt ttt ctt	2853
Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile Thr Gly Phe Leu	
420 425 430	
tcc tct gga ggg ttt ggc att gcc gct ata acc gtt ttc tct tgg att	2901
Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val Phe Ser Trp Ile	
435 440 445	
tac aag taagcacaca tttatcatct tacttcataa ttttgtgcaa tatgtgcatg	2957
Tyr Lys	
450	
catgtgttga gccagtagct ttggatcaat ttttttggtc gaataacaaa tgtaacaata	3017
agaaattgca aattctaggg aacatttggt taactaaata cgaaatttga cctagctagc	3077
ttgaatgtgt ctgtgtatat catctatata ggtaaaatgc ttggtatgat acctattgat	3137
tgtgaatagg tac gca acg gga gag cac cca cag gga tca gac aag ttg	3186
Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu	
455 460	
gac agt gca agg atg aag ttg gga agc aaa gct cag gat ctg aaa gac	3234
Asp Ser Ala Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp	
465 470 475 480	

aga gct cag tac tac gga cag caa cat act ggt ggg gaa cat gac cgt 3282
 Arg Ala Gln Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg
 485 490 495

gac cgt act cgt ggt ggc cag cac act act taagcttaat aagtatgaac 3332
 Asp Arg Thr Arg Gly Gly Gln His Thr Thr
 500 505

taaaatgcat gtaggtgtaa gagctcatgg agagcatgga atattgtatc cgaccatgta 3392
 acagtataat aactgagctc catctcactt cttctatgaa taaacaaagg atgttatgat 3452
 atattaacac tctatctatg caccttattg ttctatgata aatttcctct tattattata 3512
 aatcatctga atcgtgacgg cttatggaat gcttcaaata gtacaaaaaac aaatgtgtac 3572
 tataagactt tctaaacaat tctaacttta gcattgtgaa cgagacataa gtgttaagaa 3632
 gacataacaa ttataatgga agaagtttgt ctccatttat atattatata ttaccctactt 3692
 atgtattata ttaggatggt aaggagacat aacaattata aagagagaag tttgtatcca 3752
 tttatatatt atatactacc catttatata ttatacttat ccacttatatt aatgtcttta 3812
 taaggtttga tccatgatat ttctaataatt ttagttgata tgtatatgaa aggggtactat 3872
 ttgaactctc ttactctgta taaaggttgg atcatcctta aagtgggtct atttaatttt 3932
 attgcttctt acagataaaa aaaaaattat gagttggttt gataaaaatat tgaaggattt 3992
 aaaataataa taaataataa ataacatata atatatgtat ataaatttat tataatataa 4052
 catttatcta taaaaaagta aatattgtca taaatctata caatcgttta gccttgctgg 4112
 acgactctca attattttaa cgagagtaaa catatttgac tttttgggta tttacaaat 4172
 tattatttaa cactatatga aatttttttt ttttatcggc aaggaaataa aattaaatta 4232
 ggagggacaa tgggtgtgtcc caatccttat acaaccaact tccacaggaa ggtcaggtcg 4292
 gggacaacaa aaaaacaggc aagggaattt ttttaatttg ggttgtcttg tttgctgcat 4352
 aatttatgca gtaaaacact acacataacc ctttttagcag tagagcaatg gttgaccgtg 4412
 tgcttagctt cttttatttt atttttttat cagcaaagaa taaataaaat aaaatgagac 4472
 acttcaggga tgtttcaacc cttatacaaa accccaaaaa caagtttctt agcaccttac 4532
 caactaaggt acc 4545

<210> 19

<211> 451

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Phaseolin
 promoter-thioredoxin reductase oleosin-phaseolin
 terminator

<400> 19

Met	Asn	Gly	Leu	Glu	Thr	His	Asn	Thr	Arg	Leu	Cys	Ile	Val	Gly	Ser	1	5	10	15
Gly	Pro	Ala	Ala	His	Thr	Ala	Ala	Ile	Tyr	Ala	Ala	Arg	Ala	Glu	Leu	20	25	30	
Lys	Pro	Leu	Leu	Phe	Glu	Gly	Trp	Met	Ala	Asn	Asp	Ile	Ala	Pro	Gly	35	40	45	
Gly	Gln	Leu	Thr	Thr	Thr	Thr	Asp	Val	Glu	Asn	Phe	Pro	Gly	Phe	Pro	50	55	60	
Glu	Gly	Ile	Leu	Gly	Val	Glu	Leu	Thr	Asp	Lys	Phe	Arg	Lys	Gln	Ser	65	70	75	80
Glu	Arg	Phe	Gly	Thr	Thr	Ile	Phe	Thr	Glu	Thr	Val	Thr	Lys	Val	Asp	85	90	95	
Phe	Ser	Ser	Lys	Pro	Phe	Lys	Leu	Phe	Thr	Asp	Ser	Lys	Ala	Ile	Leu	100	105	110	
Ala	Asp	Ala	Val	Ile	Leu	Ala	Thr	Gly	Ala	Val	Ala	Lys	Arg	Leu	Ser	115	120	125	
Phe	Val	Gly	Ser	Gly	Glu	Gly	Ser	Gly	Gly	Phe	Trp	Asn	Arg	Gly	Ile	130	135	140	
Ser	Ala	Cys	Ala	Val	Cys	Asp	Gly	Ala	Ala	Pro	Ile	Phe	Arg	Asn	Lys	145	150	155	160
Pro	Leu	Ala	Val	Ile	Gly	Gly	Gly	Asp	Ser	Ala	Met	Glu	Glu	Ala	Asn	165	170	175	
Phe	Leu	Thr	Lys	Tyr	Gly	Ser	Lys	Val	Tyr	Ile	Ile	His	Arg	Arg	Asp	180	185	190	
Ala	Phe	Arg	Ala	Ser	Lys	Ile	Met	Gln	Gln	Arg	Ala	Leu	Ser	Asn	Pro	195	200	205	
Lys	Ile	Asp	Val	Ile	Trp	Asn	Ser	Ser	Val	Val	Glu	Ala	Tyr	Gly	Asp	210	215	220	
Gly	Glu	Arg	Asp	Val	Leu	Gly	Gly	Leu	Lys	Val	Lys	Asn	Val	Val	Thr	225	230	235	240
Gly	Asp	Val	Ser	Asp	Leu	Lys	Val	Ser	Gly	Leu	Phe	Phe	Ala	Ile	Gly	245	250	255	
His	Glu	Pro	Ala	Thr	Lys	Phe	Leu	Asp	Gly	Gly	Val	Glu	Leu	Asp	Ser	260	265	270	

Asp Gly Tyr Val Val Thr Lys Pro Gly Thr Thr Gln Thr Ser Val Pro
 275 280 285
 Gly Val Phe Ala Ala Gly Asp Val Gln Asp Lys Lys Tyr Arg Gln Ala
 290 295 300
 Ile Thr Ala Ala Gly Thr Gly Cys Met Ala Ala Leu Asp Ala Glu His
 305 310 315 320
 Tyr Leu Gln Glu Ile Gly Ser Gln Gln Gly Lys Ser Asp Met Ala Asp
 325 330 335
 Thr Ala Arg Gly Thr His His Asp Ile Ile Gly Arg Asp Gln Tyr Pro
 340 345 350
 Met Met Gly Arg Asp Arg Asp Gln Tyr Gln Met Ser Gly Arg Gly Ser
 355 360 365
 Asp Tyr Ser Lys Ser Arg Gln Ile Ala Lys Ala Ala Thr Ala Val Thr
 370 375 380
 Ala Gly Gly Ser Leu Leu Val Leu Ser Ser Leu Thr Leu Val Gly Thr
 385 390 395 400
 Val Ile Ala Leu Thr Val Ala Thr Pro Leu Leu Val Ile Phe Ser Pro
 405 410 415
 Ile Leu Val Pro Ala Leu Ile Thr Val Ala Leu Leu Ile Thr Gly Phe
 420 425 430
 Leu Ser Ser Gly Gly Phe Gly Ile Ala Ala Ile Thr Val Phe Ser Trp
 435 440 445
 Ile Tyr Lys
 450

<210> 20

<211> 55

<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Phaseolin
 promoter-thioredoxin reductase oleosin-phaseolin
 terminator

<400> 20

Tyr Ala Thr Gly Glu His Pro Gln Gly Ser Asp Lys Leu Asp Ser Ala
 1 5 10 15
 Arg Met Lys Leu Gly Ser Lys Ala Gln Asp Leu Lys Asp Arg Ala Gln
 20 25 30
 Tyr Tyr Gly Gln Gln His Thr Gly Gly Glu His Asp Arg Asp Arg Thr
 35 40 45

Arg Gly Gly Gln His Thr Thr
 50 55

<210> 21
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 21
 taccatggct tcggaagaag ga 22

<210> 22
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 22
 gaaagcttaa gccaaagtgt tg 22

<210> 23
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 23
 ggccagcaca ctaccatgaa tggctctgaa actcac 36

<210> 24
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 24
 ttaagcttca atcactctta ccttgctg 28